



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/641,319

Source: OIPE

Date Processed by STIC: 6-8-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/641,319

DATE: 06/08/2001

TIME: 16:49:41

Input Set : A:\04578~1.txt

Output Set: N:\CRF3\06082001\I641319.raw

Does Not Comply  
Corrected Diskette Needed

See p 6

3 <110> APPLICANT: Slater, Michael  
 4 Huang, Fen  
 5 Hartnett, James  
 7 <120> TITLE OF INVENTION: Mutant TNE Polymerases  
 9 <130> FILE REFERENCE: PRMG-04578  
 11 <140> CURRENT APPLICATION NUMBER: 09/641,319  
 C--> 12 <141> CURRENT FILING DATE: 2001-05-08  
 14 <150> PRIOR APPLICATION NUMBER: 09/385,986  
 15 <151> PRIOR FILING DATE: 1999-08-30  
 17 <150> PRIOR APPLICATION NUMBER: 08/484,661  
 18 <151> PRIOR FILING DATE: 1996-06-07  
 20 <160> NUMBER OF SEQ ID NOS: 51  
 22 <170> SOFTWARE: PatentIn version 3.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 2642  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Thermotoga neapolitana  
 29 <220> FEATURE:  
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 31 <222> LOCATION: (1)..(2679)  
 33 <400> SEQUENCE: 1  
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 35 Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala  
 36 1 5 10 15  
 38 tat tac gcc ctc gac aga tcc ctt tcc aca tcc aca gga att cca acg 96  
 39 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
 40 20 25 30  
 42 aac gcc gtc tat ggc gtt gcc agg atc ctc gtt aaa ttc ata aag gaa 144  
 43 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu  
 44 35 40 45  
 46 cac att ata ccc gaa aag gac tac gag gct ctg gcc ttc gac aag aag 192  
 47 His Ile Ile Pro Gln Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys  
 48 50 55 60  
 50 gca gcg acg ttc aga cac aaa ctg ctc gaa gcg tac aag gcg caa agg 240  
 51 Ala Ala Thr Phe Arg His Lys Leu Leu Glu Ala Tyr Lys Ala Gln Arg  
 52 65 70 75 80  
 54 cca aag acg cag gat ctt cta gtt cag cag cta cct tac atc aag cgg 288  
 55 Pro Lys Thr Pro Asp Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg  
 56 85 90 95  
 58 ctg ata gaa gct ctt ggt ttc aaa ctg ctg gag ctg gaa gga tac gaa 336  
 59 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu  
 60 100 105 110  
 62 gca gac gat atc atc gcc acg ctt gca gtc aag ggc tgc acg ttt ttt 384  
 63 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Cys Thr Phe Phe  
 64 115 120 125  
 66 gat gag att ttc ata ata acc ggt gac aag gat atg ctt caa ctt gta 432  
 67 Asp Glu Ile Phe Ile Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val

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Input Set : A:\04578~1.txt

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68	130	135	140	
70	aac gag aag ata aag gtc tgg aga atc gtc aag gga ata tcg gat ctt	440		
71	Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu			
72	145	150	155	160
74	gag ctt tac gat tcg aaa aag gty aaa gaa aga tac ggt gty gaa cca	508		
75	Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro			
76	165	170	175	
78	cat cag ata cag gat ctt cta gaa cta acg gga gag gag ata gac aac	576		
79	His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Glu Ile Asp Asn			
80	180	185	190	
82	att ccc ggt gta aag gga ata ggt gaa aag acc gat gta cag ctt ctc	624		
83	Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu			
84	195	200	205	
86	ggc aag tac aga aat ctt gaa gag att cta gag cat gac cgt gaa ctc	672		
87	Gly Lys Tyr Arg Asn Leu Glu Asp Ile Leu Glu His Ala Arg Glu Leu			
88	210	215	220	
90	ccc cag aga gty aga aag gat ctc ttg aga gac aag gaa gtt gac atc	720		
91	Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile			
92	225	230	235	240
94	ctc agt aaa aaa ctt gaa aat cty gty acg aac gaa cct gtt gaa gty	768		
95	Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val			
96	245	250	255	
98	gac tgg gaa gag atg aaa tac aga gga tac gac aag aga aaa cta ctt	816		
99	Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu			
100	260	265	270	
102	ccg ata ttg aaa gaa ctg gag ttt gat tcc atc atg aag gaa ctt caa	864		
103	Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln			
104	275	280	285	
106	ctg tac gaa gaa gca gaa ccc acc gga tac gaa ttc gty aag gat cat	912		
107	Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His			
108	290	295	300	
110	aag acc ttc gaa gat ctc atc gaa aag ctg aag aag gtt cca tct ttt	960		
111	Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe			
112	305	310	315	320
114	gcc ctg gac ctt gaa aag ttc tcc ctt gac tcg ttc aac tct gag ata	1008		
115	Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile			
116	325	330	335	
118	gtc ggc ctc tcc gty tcg ttc aaa ccg aaa cca gct tat ttc att cca	1056		
119	Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro			
120	340	345	350	
122	ctt cat cag aga aac gac cag aat ctt gat gaa cca ctg gty ctg tcg	1104		
123	Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser			
124	355	360	365	
126	aag ttg aaa gag atc ctc gaa gac ccg tct tcg aag att gty ggt cag	1152		
127	Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln			
128	370	375	380	
130	aac ctg aag tac gac tac aag gtt ctt atg gta aag ggt ata tcg cca	1200		
131	Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro			
132	385	390	395	400

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134	gtt	tat	ccg	cat	ttt	gac	acg	atg	ata	gct	gca	tat	ttg	ctg	gag	cca	1248
135	Val	Tyr	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro	
136					405					410					415		
138	aac	gag	aaa	aaa	ttc	aat	ctc	gaa	gat	ctg	tct	ttg	aaa	ttt	ctc	gga	1296
139	Asn	Glu	Lys	Lys	Phe	Asn	Leu	Glu	Asp	Leu	Ser	Leu	Lys	Phe	Leu	Gly	
140					420				425					430			
142	tac	aaa	atg	acg	tct	tat	cag	gaa	ctg	atg	tgg	ttt	tcc	tca	cca	ctt	1344
143	Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Ser	Pro	Leu	
144					435				440					445			
146	ttt	ggt	ttc	agg	ttt	gag	gat	gtt	cgg	gta	gac	aag	gct	ggg	aac	tac	1392
147	Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Asp	Lys	Ala	Ala	Asn	Tyr	
148					450				455					460			
150	tcc	tgc	gag	gat	gca	gac	atc	act	tat	agg	ctc	tac	aag	ata	ctc	agg	1440
151	Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Ile	Leu	Ser	
152	465								470					475			
154	atg	aag	ctc	cat	gaa	gag	gaa	ctt	gag	aac	gtc	ttc	tac	agg	ata	gag	1488
155	Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	Phe	Tyr	Arg	Ile	Glu	
156					485					490				495			
158	atg	ccg	ctt	gtg	aac	gtt	ctt	gaa	cag	atg	gaa	ttg	aac	ggg	gtg	tat	1536
159	Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly	Val	Tyr	
160					500					505				510			
162	gtg	gac	aca	gaa	ttc	ctg	aaa	aag	ctc	tcc	gag	gac	tac	ggg	aaa	aag	1584
163	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys	
164					515					520				525			
166	ctc	gag	gaa	ctg	gac	gaa	aaa	atc	tac	cag	ata	gca	gaa	gac	ccc	ttc	1632
167	Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile	Ala	Gly	Glu	Pro	Phe	
168					530					535				540			
170	aac	atc	aat	tct	cca	aaa	cag	gtt	tca	aag	atc	ctt	ttt	gag	aag	ctg	1680
171	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Lys	Ile	Leu	Phe	Glu	Lys	Leu	
172	545								550					555			
174	gga	ata	aaa	ccc	cgt	gga	aaa	acg	aca	aaa	aca	gga	ggg	tac	tct	acc	1728
175	Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Ala	Tyr	Ser	Thr	
176					565					570				575			
178	agg	ata	gag	gtg	ttg	gaa	gag	ata	ggg	aat	gag	cac	gag	ata	gta	ccc	1776
179	Arg	Ile	Glu	Val	Leu	Glu	Glu	Ile	Ala	Asn	Glu	His	Glu	Ile	Val	Pro	
180					580					585				590			
182	ctc	att	ctc	gag	tac	aga	aag	atc	cag	aaa	ctg	aaa	tgg	acc	tac	ata	1824
183	Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu	Lys	Ser	Thr	Tyr	Ile	
184					595					600				605			
186	gac	acc	ctt	ccg	aaa	ctt	gtg	aac	ccg	aaa	acc	gga	aga	att	cat	gaa	1872
187	Asp	Thr	Leu	Pro	Lys	Leu	Val	Asn	Pro	Lys	Thr	Gly	Arg	Ile	His	Ala	
188					610					615				620			
190	tct	ttc	cac	cag	atg	ggt	acc	gac	act	ggg	agg	ttg	agt	agg	agt	gat	1920
191	Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	
192	625									630				635			
194	cca	aat	ctt	cag	aat	ctt	ccg	aca	aag	agg	gaa	gag	gga	aaa	gaa	att	1968
195	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile	
196					645					650				655			
198	aga	aaa	ggg	att	gtg	ccc	cag	gat	cca	gac	tgg	tgg	atc	gtc	agt	ggg	2016

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199 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
200      660      685      670
202 gat tat tcc caa ata gaa ctc aga atc ctc gct cat ctc agt ggt gat 2064
203 Asp Tyr Ser Gln Ile Gln Leu Arg Ile Leu Ala His Leu Ser Gly Asp
204      675      680      685
206 gag aac ctt gtg aag gcc ttc gag gag ggc atc gat gtg cgc acc atg 2112
207 Glu Asn Leu Val Lys Ala Phe Glu Gln Gly Ile Asp Val His Thr Leu
208      690      695      700
210 act gcc tcc agt atc tac aac gta agt cca gaa gaa gtg aac gaa gaa 2160
211 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Gln Val Asn Gln Gln
212 705      710      715      720
214 atg cga cgg gtt gga aag atg gtg aac ttc tct ata ata tac agt ctc 2208
215 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
216      725      730      735
218 aca cag tac ggt ctt tct gtg aga att gga ata cag gtt aac gaa gaa 2256
219 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Gln Ala
220      740      745      750
222 gaa aag atg att atc agc cat ttc tta ctc tat cca aag gtg cga agc 2304
223 Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
224      755      760      765
226 tac atc cag cag gtt gtt gca gag gta aac gag aag gcc tac gtc agt 2352
227 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Gln Lys Gly Tyr Val Arg
228      770      775      780
230 act ctc ttt gta aga aaa aga gat att ccc cag ctc atg gca agg gac 2400
231 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
232 785      790      795      800
234 aag aac acc cag tcc gaa ggc aac aga atc gca ata aac acc acc att 2448
235 Lys Asn Thr Gln Ser Gln Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
236      805      810      815
238 cag cga acg ggg gaa gat ata ata aac ttg gct atg ata gat ata gac 2496
239 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
240      820      825      830
242 gag gag ctg aga aac aga aac atg aac tcc aga atg atc att cag gtt 2544
243 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
244      835      840      845
246 cat gac gaa ctg gtc ttc gag gtt ccc gat gag gaa aac gaa gaa cta 2592
247 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
248      850      855      860
250 gtt gat ctg gtg aag aac aaa atg aca aat gtg gtg aac ctc tct gtg 2640
251 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
252 865      870      875      880
254 cct ctt gag gtt gac ata agc atc gga aac agc tgg tct tga 2682
255 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
256      885      890
259 210 - SEQ ID NO: 2
260 211 - LENGTH: 893
261 212 - TYPE: PRT
262 213 - ORGANISM: Thermotoga neapolitana
264 400 - SEQUENCE: 2

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Output Set: N:\CRF3\06082001\I641319.raw

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266 Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
267 1 5 10 15
270 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
271 20 25 30
274 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
275 35 40 45
278 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
279 50 55 60
282 Ala Ala Thr Phe Arg His Lys Leu Leu Glu Ala Tyr Lys Ala Gln Arg
283 65 70 75 80
286 Pro Lys Thr Pro Asp Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
287 85 90 95
290 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
291 100 105 110
294 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Cys Thr Phe Phe
295 115 120 125
298 Asp Glu Ile Phe Ile Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
299 130 135 140
302 Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
303 145 150 155 160
306 Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
307 165 170 175
310 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Glu Ile Asp Asn
311 180 185 190
314 Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
315 195 200 205
318 Gly Lys Tyr Arg Asn Leu Glu Asp Ile Leu Glu His Ala Arg Glu Leu
319 210 215 220
322 Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
323 225 230 235 240
326 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
327 245 250 255
330 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
331 260 265 270
334 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
335 275 280 285
338 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
339 290 295 300
342 Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
343 305 310 315 320
346 Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Arg Cys Glu Ile
347 325 330 335
350 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
351 340 345 350
354 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser
355 355 360 365
358 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln
359 370 375 380
362 Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro

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04/046, 319

p 6.

<210> 3  
<211> 44  
<212> DNA  
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<220>  
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<223> Synthetic

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44

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<400> 4  
aggccagggc tgtgccatca aagagaaata gtctcgc

Invalid <213> response.  
Artificial sequence and unknown  
are separate responses. You  
may use only one. It  
must be accompanied by  
37  
<220>, <223> features.

<210> 5  
<211> 39  
<212> DNA  
<213> Artificial/Unknown

<220>  
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<223> Synthetic

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39

Please Note

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

## VERIFICATION SUMMARY

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Input Set : A:\04578~1.txt

Output Set: N:\CRF3\06082001\I641319.raw

L:112 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:493 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:597 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:511 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:535 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:549 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:723 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:895 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
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L:1089 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
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L:1991 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22  
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L:2516 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26  
L:2683 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27  
L:2697 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28  
L:2869 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29  
L:2936 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30  
L:2950 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31  
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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/641,319

DATE: 06/08/2001

TIME: 16:49:42

Input Set : A:\04578~1.txt

Output Set: N:\CRF3\06082001\I641319.raw

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